Figure 1: 121P1F1 SSH sequence of 254 nucleotides (SEQ ID: 1)

```
  1 GATCACAGTC TTTGTATTTT TCTAGTTCTG CCTTTAGCTG TTCCCTTTGG TCTCGAAGTG
 61 AAGAAAAGCT CTTTTGCTAGC CTGGTTCGCT CTTCCGTTTC ACATCGGCCA ATTTTAGCTT
121 TCTCAATGCT TTTCTGTAGG CTTGCATGCT TTTGACTTCC CTCAGACAAC TGAGATTCCA
181 GAACCTCCAA CTTATGTTTC CTTGCATGAA GAGCTTTACT TGGAAAAGCC CAATAATAAT
241 TAGAAGTTCC GATC
```

Figure 2: The cDNA and Amino Acid Sequence(s)

Figure 2A. The cDNA (SEQ ID. NO. : 2) and amino acid sequence (SEQ ID. NO. : 3) of 121P1F1. The start methionine is underlined. The open reading frame extends from nucleic acid 82-699 including the stop codon.

```
   1 ccaaaatcaaacggcgtccgggcctgtcccgccctctcccaagcgcgggccccggccagcc
   1                          M  S  K  K  K  G  L  S  A  E  E  K  K
  61 ggaagccccctgcgccccgccgccATGTCAAAGAAAAAAGGACTGAGTGCAGAAGAAAAGAAGA
  14 T  R  M  M  E  I  F  S  E  T  K  D  V  F  Q  L  K  D  L  E
 121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
  34 K  I  A  P  K  E  K  G  I  T  A  M  S  V  K  E  V  L  Q  S
 181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC
  54 L  V  D  D  G  M  V  D  S  E  R  I  G  T  S  N  Y  Y  W  A
 241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACTTCTAATTATTATTGGGCT
  74 F  P  S  K  A  L  H  A  E  K  H  R  L  E  V  L  E  S  Q  L
 301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
  94 S  E  G  S  Q  K  H  A  S  D  Q  R  S  I  E  K  A  K  I  G
 361 TCTGAGGGAAGTCAAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
 114 R  C  E  T  E  E  R  T  R  L  A  F  E  L  S  S  L  S  D  Q
 421 CGATGTGAAACGGAAGAGCGAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAA
 134 R  E  Q  L  K  A  E  V  E  K  Y  K  D  C  D  P  Q  V  V  E
 481 AGGGAACAGCTAAAGGCAGAAGTAGAAAAATACAAAGACTGTGATCCGCAACTTGTGGAA
 154 E  I  E  Q  A  N  K  V  A  K  E  A  A  N  E  W  T  D  N  I
 541 GAAATAGGCCAAGCAAATAAAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATA
 174 F  A  I  K  S  W  A  K  E  K  F  G  F  E  E  N  K  I  D  E
 601 TTCGCAATAAAATCTTGGGCCAAAAGAAAATTTGGGTTTGAAGAAAATAAAATTGATAGA
 194 T  F  G  I  F  E  D  F  D  Y  I  D  *
 661 ACTTTTGGAATTCCAGAAGACTTTGACTACATAGACTAAAatattccatggtggtgaagg
 721 atgtacaagcttgtgaatatgtaaattttaaactattatctaactaagtgtactgaattg
```

781 tcgtttgcctgtaactgtgtttatcattttattaatgttaaataaagtgtaaaatgcaaa

841 aaaaaaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. : 4) and amino acid sequence (SEQ ID. NO. : 5) of 121P1F1 splice variant 1A. The start methionine is underlined. The open reading frame extends from nucleic acid 82-462 including the stop codon.

```
    1 ccaaaatcaaaacgcgtccgggcctgtccgcccctctccccaagcgcgggcccggccagc
  1                         M  S  K  K  K  G  L  S  A  E  E  K  R
 61 ggaagccccctgcgccccgcgccATGTCAAAGAAAAAAGGACTGAGTGCAGAAGAAAAGAGA
 14 T  R  M  M  E  I  F  S  E  T  K  D  V  F  Q  L  K  D  L  E
121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
 34 K  I  A  P  K  E  K  G  I  T  A  M  S  V  K  E  V  L  Q  S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC
 54 L  V  D  D  G  M  V  D  C  E  F  I  G  T  S  N  Y  Y  W  A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACTTCCTAATTATTATTGGGCT
 74 F  P  S  K  A  L  H  A  R  K  H  K  L  E  V  L  E  S  Q  D
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGGAC
 94 P  G  C  C  F  H  E  I  I  K  V  S  Y  Y  P  K  F  W  L  G
361 CCTGGCTGCTGCTTCCATGAAATAATTAAAGTCTCCTATTATAGAAAATTCTGGCTGGGC
114 A  V  A  H  A  C  N  P  S  T  L  G  G  *
421 GCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAggcgggcagatcacgagg
481 tgacttttccccacccccacatgaaagtgcaagatggagttgtctgagggaagtcaaaagc
541 atgcaagcctacagaaaagcattgagaaagctaaaattggccgatgtgaaacggaagagc
601 gaaccaggctagcaaaagagctttcttcacttcgagacccaaagggaacagctaaaggcag
661 aagtagaaaaatacaaagactgtgatccgcaagttgtggaagaaatacgccaagcaaata
721 aagtagccaaagaaagctgctaacagatggactgataacatattcgcaataaaatcttggg
781 ccaaaagaaaatttgggtttgaagaaaataaaattgatagaacttttggaattccagaag
841 actttgactacatagactaaaatattccatggtggtgaaggatgtacaagcttgtgaata
901 tgtaaattttaaactattatctaactaagtgtactgaattgtcgtttgcctgtaactgtg
961 tttatcattttattaatgttaaataaagtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaa
1021 aaaaaaaa
```

Figure 2C. The cDNA (SEQ ID. NO. : 6) and amino acid sequence (SEQ ID. NO. : 7) of 121P1F1 splice variant 1B. The start methionine is underlined. The open reading frame extends from nucleic acid 501-860 including the stop codon.

```
       1 ccaaaatcaaacgcgtccgggcctgtcccgcccctctccccaagcgcgggccccggccagc
      61 ggaagccccctgcgcccgcgccatgtcaaagaaaaaaggactgagtgcagaagaaaagaga
     121 actcgcatgatggaaatattttctgaaacaaaagatgtatttcaattaaaagacttggag
     181 aagattgctcccaaagagaaaggcattactgctatgtcagtaaaagaagtccttcaaagc
     241 ttagttgatgatggtatggttgactgtgagaggatcggaacttctaatttattgggct
     301 tttccaagtaaagctcttcatgcaaggaaacataagttggaggttctggaatctcaggac
     361 cctggctgctgcttccatgaaataatttaaagtctcctattatagaaaaattctggctgggc
     421 gcagtggctcacgcctgtaatcccagcactttgggaggctgaggcgggcagatcacgagg
       1                       M  K  C  K  M  E  L  S  E  G  S  Q  K  H
     481 tgactttccccccaccccccacATGAAGTGCAAGATGGAGTTGTCTGAGGGAAGTCAAAAGC
      15  A  S  L  Q  K  S  I  E  K  A  K  I  S  R  C  E  T  E  E  R
     541 ATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGC
      35  T  R  L  A  K  E  L  S  S  L  R  D  Q  R  E  Q  L  K  A  E
     601 GAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAAAGGGAACAGCTAAAGGCAG
      55  V  E  K  Y  K  D  C  D  P  Q  V  V  E  E  I  R  Q  A  N  K
     661 AAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATACGCCAAGCAAATA
      75  V  A  K  E  A  A  N  R  W  T  D  N  I  F  A  I  K  S  W  A
     721 AAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATATTCGCAATAAAATCTTGGG
      95  K  R  K  F  S  F  E  E  N  K  I  D  R  T  F  G  I  P  E  D
     781 CCAAAAGAAAATTTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGGAATTCCAGAAG
     115  F  D  Y  I  D  *
     841 ACTTTGACTACATAGACTAAaatattccatggtggtgaaggatgtacaagcttgtgaata
     901 tgtaaattttaaactattatctaactaagtgtactgaattgtcgtttgcctgtaacctgtg
     961 tttatcattttattaatgttaaataaagtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaa
    1021 aaaaaaaa
```

Figure 2D. The cDNA (SEQ ID. NO. : 8) and amino acid sequence (SEQ ID. NO. : 9) of 121P1F1 splice variant 2. The start methionine is underlined. The open reading frame extends from nucleic acid 82-450 including the stop codon.

```
   1 ccaaaatcaaacgcgtccgggcctgtccctgccctctcccccaagcgcgggcccggccagc
   1                         M  S  K  K  K  G  L  S  A  E  E  K  R
  61 ggaagccccctgcgccccgcgccATGTCAAAGAAAAAAGGACTGAGTGCAGAAGAAAAGAGA
  14 T  R  M  M  E  I  F  S  E  T  K  D  V  F  Q  L  K  D  L  E
 121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
  34 K  I  A  P  K  E  K  G  I  T  A  M  S  V  K  E  V  L  Q  S
 181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC
  54 L  V  D  D  G  M  V  D  C  E  E  I  G  F  S  N  Y  Y  W  A
 241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACTTCTAATTATTATTGGGCT
  74 F  P  S  K  A  L  H  A  R  K  H  K  L  E  V  L  E  S  Q  L
 301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
  94 S  E  G  S  Q  K  H  A  S  L  Q  K  S  I  E  K  A  K  I  G
 361 TCTGAGGGAAGTCAAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
 114 P  C  E  T  A  K  Q  I  K  *
 421 CGATGTGAAACGGCCAAGCAAATAAAGTAGccaaagaagctgctaacagatggactgata
 481 acatattcgcaataaaatcttgggccaaaagaaaatttgggtttgaagaaaataaaattg
 541 atagaacttttggaattccagaagactttgactacatagactaaaatattccatggtggt
 601 gaaggatgtacaagcttgtgaatatgtaaattttaaactattatctaactaagtgtactg
 661 aattgtcgtttgcctgtaactgtgtttatcattttattaatgttaaataaagtgtaaaat
 721 gcaaaaaaaaaaaaaaaaaaaaaaaaaaaa
```

Figure 2E. The cDNA (SEQ ID. NO. : 10) and amino acid sequence (SEQ ID. NO. : 11) of 121P1F1 splice variant 3. The start methionine is underlined. The open reading frame extends from nucleic acid 82-654 including the stop codon.

```
    1 ccaaaatcaaacgcgtccgggcctgtcccgccccctctccccaagcgcgggcccggccagc
    1                         M  S  K  K  K  G  L  S  A  E  E  K  R
   61 ggaagccccctgcgcccgcgccATGTCAAAGAAAAAAGGACTGAGTGCAGAAGAAAAGAGA
   14 T  R  M  M  E  I  F  S  E  T  K  L  V  F  Q  L  K  D  L  E
  121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
   34 K  I  A  P  K  E  K  G  I  T  A  M  S  V  K  E  V  L  Q  S
  181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC
   54 L  V  D  D  G  M  V  D  C  E  P  I  G  T  S  N  Y  Y  W  A
  241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACTTCTAATTATTATTGGGCT
   74 F  P  S  K  A  L  H  A  R  K  H  K  L  E  V  L  E  S  Q  L
  301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
   94 S  E  G  S  Q  K  H  A  S  L  Q  K  S  I  E  K  A  K  I  G
  361 TCTGAGGGAAGTCAAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
  114 E  C  E  T  E  E  R  T  E  L  A  K  E  L  S  S  L  R  D  Q
  421 CGATGTGAAACGGAAGAGCGAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAA
  134 E  E  Q  L  K  A  E  V  E  K  Y  K  E  C  D  P  Q  V  V  E
  481 AGGGAACAGCTAAAGGCAGAAGTAGAAAAATACAAAGAGTGTGATCCGCAAGTTGTGGAA
  154 E  I  H  N  I  F  A  I  K  S  W  A  K  R  K  F  G  F  E  E
  541 GAAATACATAACATATTCGCAATAAAATCTTGGGCAAAAGAAAATTTGGGTTTGAAGAA
  174 N  K  I  D  R  T  F  G  I  P  E  D  F  D  Y  I  D  *
  601 AATAAAATTGATAGAACTTTTGGAATTCCAGAAGACTTTGACTACATAGACTAAaatatt
  661 ccatggtggtgaaggatgtacaagcttgtgaatatgtaaattttaaactattatctaact
  721 aagtgtactgaattgtcgtttgcctgtaactgtgtttatcattttattaatgttaaataa
  781 agtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
```

Figure 2F. The cDNA (SEQ ID. NO. : 12) and amino acid sequence (SEQ ID. NO. : 13) of 121P1F1 splice variant 4. The start methionine is underlined. The open reading frame extends from nucleic acid 281-853 including the stop codon.

```
   1 gttttctgtattgtaatatgtagagcacattccagaactgctcagtttcgagttacctaa
  61 tggatcttcactgtgtgccaatttagtcgatttctgtgaaaacgccccggtttctgccaaa
 121 gggcaggagtcgctjctcttgtgccgggtgctactggttgtgtagggcgctgttgcttct
 181 ttaaggacgctct,actgaattaggcttcctcgtgggtcatgatcaattaagtcctgtc
   1                                                M  M  E  I  F  S  E
 241 aaagaaaaaaggtt.gagtgccacaagaaaagagaaactcgcATGATGGAAATATTTTCTGA
   8  T  K  D  V  F  Q  L  F  D  L  E  K  I  A  F  K  E  K  G  I
 301 AACAAAAGATGTATTTCAATTAAAAGACTTGGAGAAGATTGCTCCCAAAGAGAAAGGCAT
  28  T  A  M  S  V  F  E  V  L  Q  S  L  V  D  E  G  M  V  D  C
 361 TACTGCTATT TAGTAAAAGAAGTCTTTCAAAGCTTAGTTGATGATGGTATGGTTGACTG
  48  E  F  T  G  T  S  N  Y  Y  W  A  F  P  S  K  A  L  H  A  F
 421 TGAGAGGATCGGAACTTCTAATTATTATTGGGCTTTTCCAAGTAAAGCTCTTCATGCAAG
  68  K  K  K  L  E  V  L  E  S  Q  L  S  E  G  S  Q  K  H  A  S
 481 GAAACATAAGTTGGAGGTTCTGGAATCTCAGTTGTCTGAGGGAAGTCAAAAGCATGCAAG
  88  L  Q  K  S  I  E  F  A  K  I  G  F  D  E  T  E  E  R  T  R
 541 CTTACAGAAAACCATTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGCGAACCAG
 108  L  A  K  E  L  S  S  L  R  I  Q  R  E  Q  L  K  A  E  V  E
 601 GCTAGCAAAAGAGCTTTCTTCATTTCGAGACCAAAGGGAACAGCTAAAGGCAGAAGTAGA
 128  K  Y  K  D  L  D  F  Q  V  V  E  E  I  F  Q  A  N  K  V  A
 661 AAAATACAAAGACTGTGATCCGCAAGTTCTGGAAGAAATACGCCAAGCAAATAAAGTAGC
 148  K  E  A  A  N  E  W  T  D  N  I  F  A  I  K  S  W  A  K  E
 721 CAAAGAAGCTGCTAACAGATGGACTGATAACATATTCGCAATAAAATCTTGGGCCAAAAG
 168  K  F  G  T  E  E  N  K  I  D  K  T  F  S  I  P  E  D  F  I
 781 AAAATTTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGGAATTCCAGAAGACTTTGA
 188  Y  I  D  *
 841 CTACATAGACTAAaatatttccatggtggtgaaggatgtacaagcttgtgaatatgtaaat
 901 ttaaaactattatctaactaagtgtactgaattgtcgtttgcctgtaactgtgttatca
 961 ttttattaatgtaaaataaagtgtaaaatgcagatgttcttcaccctttggtaaaaca
1021 aaagcaggatgataaccatatccccccgtgctcatcaaagtaggacactaaaaatccat
1081 ccatctcagccaaagtcgagcggcgcgaatttagtagtagtagcggcgctctagagga
1141 tccaagctacgtacgcgtgcatgcgacgtcatagctcttctatagtgtcacctaaattc
1201 aagtt
```

Figure 3:

Figure 3A. Amino acid sequence of 121P1F1 (SEQ ID. NO. : 14). The 121P1F1 protein has 205 amino acids.

```
  1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
 61 DCEFIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEES
121 TRLAKELSSL RDQREQLKAE VEKYFDCDPQ VVEEIRQANK VAKEAANRWT DNIFAIKSWA
181 KRKFGFEENK IDFTFGIPED FDYID
```

Figure 3B. Amino acid sequence of 121P1F1 splice variant 1A (SEQ ID. NO. : 15). The 121P1F1 splice variant 1A protein has 126 amino acids.

```
  1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
 61 DCEFIGTSNY YWAFPSKALH ARKHKLEVLE SQDPGCCFHE IIKVSYYRKF WLGAVAHACN
121 PSTLGG
```

Figure 3C. Amino acid sequence of 121P1F1 splice variant 1B (SEQ ID. NO. : 16). The 121P1F1 splice variant 1B protein has 119 amino acids.

```
  1 MKCKMELSEG SQKHASLQKS IEKAKIGRCE TEERTFLAKE LSSLRDQREQ LKAEVEKYKD
 61 CDPQVVEEIR QANKVAKEAA NRWTDNIFAI KSWAKRKFGF EENKIDRTFG IPEDFDYID
```

Figure 3D. Amino acid sequence of 121P1F1 splice variant 2 (SEQ ID. NO. : 17). The 121P1F1 splice variant 2 protein has 122 amino acids.

```
  1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
 61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETAKQ
121 IK
```

Figure 3E. Amino acid sequence of 121P1F1 splice variant 3 (SEQ ID. NO. : 18). The 121P1F1 splice variant 3 protein has 190 amino acids.

```
  1 MSKKKGLSAE EKRTPMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
 61 DCERIGTSNY YWAFPSKALH ARKHFLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEER
121 TRLAKELSSL RDQREQLKAE VEKYKDCDPQ VVEEIHNIFA IKSWAKFKFG FEENKIDRTF
181 GIPEDFDYIL
```

Figure 3F. Amino acid sequence of 121P1F1 splice variant 4 (SEQ ID. NO. : 19). The 121P1F1 splice variant 4 protein has 190 amino acids.

```
  1 MMEIFSETKD VFQLKDLEKI APKEKGITAM SVKEVLQSLV DDGMVDCERI GTSNYYWAFP
 61 SKALHARKHF LEVLESQLSE GSQKHASLQK SIEKAKIGRC ETEERTRLAK ELSSLRDQRE
121 QLKAEVEKYK DCDPQVVEEI RQANKVAKEA ANRWTDNIFA IKSWAKFKFG FEENKIDRTF
181 GIPEDFDYIL
```

Figure 4A

Amino Acid Alignments.

Alignment of 121P1F1 protein and its variants.

A) CLUSTAL W alignment of 121P1F1 and variants 1-3. (SEQ ID NOs: 3, 5, 7, 9 and 11)

```
121P1F01          ----------MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAKKEKGITAMSVKE
sv1A              ----------MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAKKEKGITAMSVKE
sv1B              ----------MKCKMELSEGSQKHASLQKSIEKAKIGKCETEEKTRLAKELSSLKDQKE
sv-2              ----------MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAKKEKGITAMSVKE
sv-3              ----------MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAKKEKGITAMSVKE

121P1F01          VLQSLVDDGMVDCEKIGTSNYYWAFESKALHAKKHKLEVLESQLSEGSQK-HASLQKS-I
sv1A              VLQSLVDDGMVDCEKIGTSNYYWAFESKALHAKKHKLEVLESQDK-GCCK-HEIIKVSYY
sv1B              QLKAEVEK-YKDCDKQVVEEIRQANKVAKEAANKWTDNIFAIKSWAKRKFGFEENKID--
sv-2              VLQSLVDDGMVDCEKIGTSNYYWAFESKALHAKKHKLEVLESQLSEGSQK-HASLQKS-I
sv-3              VLQSLVDDGMVDCEKIGTSNYYWAFESKALHAKKHKLEVLESQLSEGSQK-HASLQKS-I

121P1F01          EKAKIGKCETEEKTRLAKELSSLKDQREQLKAEVEKYKDCDKQVVEEIKQANKVAKEAAN
sv1A              KKKWLGAVAHACNKSTLGG----------------------------------------
sv1B              KTKGIKEDKDYID----------------------------------------------
sv-2              EKAKIGKCETAKQIK--------------------------------------------
sv-3              EKAKIGKCETEEKTRLAKELSSLKDQREQLKAEVEKYKDCDKQVVEEIHNIFAIKSWAKR

121P1F01          KWTDNIFAIKSWAKRKFGFEENKIDKTFGIPEDFDYID
sv1A              ---------------------------------------
sv1B              ---------------------------------------
sv-2              ---------------------------------------
sv-3              KFGKEENKIDKTFGIPEDFDYID----------------
```

Figure 4B

Clustal alignment of 121P1F1 and variants 1A and 4 (SEQ ID Nos: 3, 13 and 5)

```
121P1F01  MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAKKEKGITAMSVKELQSLVDDGMVDCEKIGTSNYYWAFESKALHAKKHKLEVLESQLSEGSQKHASLQKSIEKAKIGKCETEEKTRLAKELSSLKDQKE
sv-4      ----------MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAKKEKGITAMSVKELQSLVDDGMVDCEKIGTSNYYWAFESKALHAKKHKLEVLESQLSEGSQKHASLQKSIEKAKIGKCETEEKTRLAKELSSLKDQKE
sv-1A     MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAKKEKGITAMSVKELQSLVDDGMVDCEKIGTSNYYWAFESKALHAKKHKLEVLESQLSEGSQKHASLQKSIEKAKIGKCETEEKTRLAKELSSLKDQKE

121P1F01  QQLKAEVEKYKDCDKQVVEEIKQANKVAKEAANKWTDNIFAIKSWAKRKFGFEENKIDKTFGIPEDFDYID
sv-4      QQLKAEVEKYKDCDKQVVEEIKQANKVAKEAANKWTDNIFAIKSWAKRKFGFEENKIDKTFGIPEDFDYID
sv-1A     QQLKAEVEKYKDCDKQVVEEIKQANKVAKEAANKWTDNIFAIKSWAKRKFGFEENKIDKTFGIPEDFDYID

121P1F01  KKKFGFEENKIDKTFGIPEDFDYID
sv-4      KKKFGFEENKIDKTFGIPEDFDYID
sv-1A     ---------- ---------- ---
```

Figure 4C

C) Alignment of [illegible] and variant [illegible] (SEQ ID NO: 20) **Alignment with human GAJ (SEQ ID NO 21)**

Identities = 205/205 (100%), Positives = 205/205 (100%)

```
121P1: 1   MSFFFGLSAEEFFTFMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
           MSFFFGLSAEEFFTFMMEIFSETKDVFQLFDLEKIAPKEKGITAMSVFEVLQSLVDDGMV
Sbjct: 1   MSFFFGLSAEEFFTFMMEIFSETKDVFQLFDLEKIAPKEKGITAMSVFEVLQSLVDDGMV 60

121P1: 61  DCEFIGTSNYYWAFPSFALHAFFHFLEVLESQLSEGSQKHASLQKSIEFAFIGFCETEEF 120
           DCEFIGTSNYYWAFPSFALHAFFHFLEVLESQLSEGSQKHASLQKSIEFAFIGFCETEEF
Sbjct: 61  DCEFIGTSNYYWAFPSFALHAFFHFLEVLESQLSEGSQKHASLQKSIEFAFIGFCETEEF 120

121P1: 121 TFLAFELSSLFDQFEQLFAEVEFYFDCDFQVVEEIFQANKVAKEAANFWTDNIFAIFSWA 180
           TFLAFELSSLFDQFEQLFAEVEFYFDCDFQVVEEIFQANKVAKEAANFWTDNIFAIFSWA
Sbjct: 121 TFLAFELSSLFDQFEQLFAEVEFYFDCDFQVVEEIFQANKVAKEAANFWTDNIFAIFSWA 180

121P1: 181 FFFFGFEENFIDFTFGIPEDFDYID 205
           FFFFGFEENFIDFTFGIPEDFDYID
Sbjct: 181 FFFFGFEENFIDFTFGIPEDFDYID 205
```

Figure 4D

D) Alignment of 121P1F and variant 1 (SEQ ID NO 22) with closest mouse homolog, a hypothetical 24.2 KDa protein. (SEQ ID NO 23)

Identities = 183/205 (89%), Positives = 193/205 (93%)

```
121P1:   1   MSKKKGLSAEEKRTRMMEIFSETKDVFQLKLLEFIAFKEKGITAMSVKEVLQSLVDDGMV  60
             MSKK+GLS EEKRTRMMEIF ETKDVFQLKLLEK+AFKEKGITAMSVKEVLQSLVDDGMV
Sbjct:   1   MSKKRGLSGEEKRTRMMEIFFETKDVFQLKLLEKLAFKEKGITAMSVKEVLQSLVDDGMV  60

121P1:  61   DCERIGTSNYYWAFPSKALHAFKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER  120
             DCERIGTSNYYWAFPSKALHAFK KLE L SQLSEGSQKHA LQKSIEKA++GR ETEER
Sbjct:  61   DCERIGTSNYYWAFPSKALHAFKRKLEALNSQLSEGSQKHADLQKSIEKARVGRQETEER  120

121P1: 121   TFLAKELSSLFDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANEWTDNIFAIKSWA  180
               LAKEL S FDQR+QLKAEVEKY++CDPQVVEEIR+ANKVAKEAANEWTDNIFAIKSWA
Sbjct: 121   AMLAKELFSFFDQRQQLKAEVEKYRECDPQVVEEIREANKVAKEAANEWTDNIFAIKSWA  180

121P1: 181   KKKFGFEENKIDFTFGIPEDFDYID  205
             KKKFGFEE+KID+ FGIPEDFDYID
Sbjct: 181   KKKFGFEESKIDFNFGIPEDFDYID  205
```

Figure 4E

E. Alignment of [illegible] and variant (SEQ ID NO: [illegible])

```
with>gi|1175412|sp|Q09739|YA53_SCHPO HYPOTHETICAL 24.2 KD PROTEIN
C13A11.03 IN CHROMOSOME I                              :
 gi|7490680|pir||T37d10 hypothetical coiled-coil protein - fission yeast
 (Schizosaccharomyces pombe)
  gi|984224|emb|CAA90804.1| (Z54096) hypothetical coiled-coil protein
 [Schizosaccharomyces pombe]
          Length = 210

 Score =  121 bits (305), Expect = 5e-27
 Identities = 81/202 (40%), Positives = 115/202 (56%), Gaps = 6/202 (2%)

Query: 5    KGLSAEEKRTFMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER 64
             KGLS  EKR F+  IF ++KD FQLK++EK+  K K I   +VK+VLQSLVDD +V  E+
Sbjct: 4    KGLSLAEKRRFLEAIFHDSKDFFQLKEVEKLGSK-KQIVLQTVKDVLQSLVDDNIVKTEK 62

Query: 65   IGTSNYYWAFPSKALHAEKHKLEVLESQLSEGSQKHASLQKSIEKAKIGR----CETEER 120
             IGTSNYYW+FPS A  +F+  L  L++QL +  QK  +L ++I   K  R     E +
Sbjct: 63   IGTSNYYWSFPSDAKRSRESVLGALQAQLDDLKQKSKTLDENISFEKSKRDNEGTENDAN 122

Query: 121  TRLAKELSSLFDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANFWTDNIFAIKSWA 180
                + L +   + + LK ++     C+P+  E   +  K   EAAN WTD I  + ++
Sbjct: 123  QYTLELLHAKESELKLLKTQLSNLNHCNPETFELKNENTKKYMEAANLWTDQIHTLIAFC 182

Query: 181  KFKFGFEENKIDETFGIPEDFD 202
              F  G + N+I     IPED D
Sbjct: 183  -FDMGADTNQIREYCSIPEDLD 203
```